

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:
(A) NAME: Federal Republic of Germany, ultimately represented by the Director of the Robert-Koch-Institut
(B) STREET: Nordufer 20
(C) CITY: Berlin
10 (D) STATE OR PROVINCE: Berlin
(E) COUNTRY: Germany
(F) POSTAL CODE: 13353

15 (ii) TITLE OF INVENTION: Costimulating polypeptide of T cells, monoclonal antibodies, and the preparation and use thereof

(iii) NUMBER OF SEQUENCES: 4

20 (iv) COMPUTER-READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:
APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO: 1:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2641 base pairs
(B) TYPE: Nucleotides
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40 CGAGAGCCTG AATTCAGTGT CAGCTTTGAA CACTGAACGC GAGGACTGTT AACTGTTTCT 60
GGCAAACATG AAGTCAGGCC TCTGGTATTT CTTTCTCTTC TGCTTGCGCA TTAAGTTTT 120
AACAGGAGAA ATCAATGGTT CTGCCAATTA TGAGATGTTT ATATTTTACA ACGGAGGTGT 180
ACAAATTTTA TGCAAATATC CTGACATTGT CCAGCAATTT AAAATGCAGT TGCTGAAAGG 240
GGGGCAAATA CTCTGCGATC TACTAAGAC AAAAGGAAGT GGAAACACAG TGTCCATTAA 300
GAGTCTGAAA TTCTGCCATT CTCAGTTATC CAACAACAGT GTCTCTTTT TTCTATACAA 360
CTTGGACCAT TCTCATGCCA ACTATTACTT CTGCAACCTA TCAATTTTGT ATCCTCCTCC 420
TTTTAAAGTA ACTCTTACAG GAGGATATTT GCATATTTAT GAATCACAAC TTTGTTGCCA 480
GCTGAAGTTC TGGTTACCCA TAGGATGTGC AGCCTTTGTT GTAGTCTGCA TTTTGGGATG 540
CATACTTATT TGTTGGCTTA CAAAAAGAA GTATTCATCC AGTGTGCACG ACCCTAACGG 600

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TGAATACATG TTCATGAGAG CAGTGAACAC AGCCAAAAA TCTAGACTCA CAGATGTGAC	660
CCTATAATAT GGAACCTCTGG CACCCAGGCA TGAAGCACGT TGGCCAGTTT TCCTCAACTT	720
GAAGTGCAAG ATTCTCTTAT TTCCGGGACC ACGGAGAGTC TGACTTAACT ACATACATCT	780
TCTGCTGGTG TTTTGTTCAG TCTGGAAGAA TGAAGTATC AGTCAATGGG GATTTTAAAC	840
GACTGCTTG GTACTGCCGA GTCCTCTCAA AACAAACACC CTCTTGCAAC CAGCTTTGGA	900
GAAAGCCAG CTCCTGTGTG CTCCTGGGA GTGGAATCCC TGTCTCCACA TCTGCTCCTA	960
GCAGTGCATC AGCCAGTAAA ACAACACAT TTACAAGAAA AATGTTTTAA AGATGCCAGG	1020
GGTACTGAAT CTGCAAAGCA AATGAGCAGC CAAGGACCAG CATCTGTCCG CATTCTACTA	1080
TCATACTACC TCTTCTTCT GTAGGGATGA GAATTCCTCT TTTAATCAGT CAAGGGAGAT	1140
GCTTCAAAGC TGGAGCTATT TTATTTCTGA GATGTTGATG TGAAGTGTAC ATTAGTACAT	1200
ACTCAGTACT CTCCTTCAAT TGCTGAACCC CAGTTGACCA TTTTACCAAG ACTTTAGATG	1260
CTTTCTTGTG CCCTCAATTT TCTTTTAAA AATACTTCTA CATGACTGCT TGACAGCCCA	1320
ACAGCCACTC TCAATAGAGA GCTATGTCTT ACATTCTTTC CTCTGCTGCT CAATAGTTTT	1380
ATATATCTAT GCATACATAT ATACACACAT ATGTATATAA AATTCATAAT GAATATATTT	1440
GCCTATATTC TCCCTACAAG AATATTTTG CTCCAGAAAG ACATGTTCTT TTCTCAAATT	1500
CAGTTAAAT GGTTTACTTT GTTCAAGTTA GTGGTAGGAA ACATTGCCCG GAATTGAAAG	1560
CAAATTTATT TTATTATCCT ATTTTCTACC ATTATCTATG TTTTCATGGT GCTATTAATT	1620
ACAAGTTTAG TTCTTTTGT AGATCATATT AAAATTGCAA ACAAAATCAT CTTTAATGGG	1680
CCAGCATTCT CATGGGGTAG AGCAGAATAT TCATTTAGCC TGAAAGCTGC AGTTACTATA	1740
GGTTGCTGTC AGACTATACC CATGGTGCCT CTGGGCTTGA CAGGTCAAAA TGGTCCCCAT	1800
CAGCCTGGAG CAGCCCTCCA GACCTGGGTG GAATTCCAGG GTTGAGAGAC TCCCCTGAGC	1860
CAGAGGCCAC TAGGTATTCT TGCTCCCAGA GGCTGAAGTC ACCCTGGGAA TCACAGTGGT	1920
CTACCTGCAT TCATAATTCC AGGATCTGTG AAGAGCACAT ATGTGTCAGG GCACAATTCC	1980
CTCTCATAAA AACCACACAG CCTGGAAATT GGCCCTGGCC CTTCAAGATA GCCTTCTTTA	2040
GAATATGATT TGGCTAGAAA GATTCTTAAA TATGTGGAAT ATGATTATTC TTAGCTGGAA	2100
TATTTTCTCT ACTTCCTGTC TGCATGCCCA AGGCTTCTGA AGCAGCCAAT GTCGATGCAA	2160
CAACATTTGT AACTTTAGGT AAAGTGGAT TATGTTGTAG TTTAACATTT TGTAAGTGTG	2220
TGCTTATAGT TTACAAGTGA GACCCGATAT GTCATTATGC ATACTTATAT TATCTTATGC	2280
ATGTGTAATG CTGGATGTGT ACAGTACAGT ACTGAACTTG TAATTTGAAT CTAGTATGCT	2340
GTTCTGTTTT CAGCTGACTT GGACAACCTG ACTGGCTTTG CACAGGTGTT CCCTGAGTTG	2400
TTTGACGGTT TCTGTGTGTG GGGTGGGGTA TGGGGAGGAG AACCTTCATG GTGGCCCAAC	2460
TGGCCTGGTT GTCCAAGCTG TGCCTCGACA CATCCTCATC CCCAGCATGG GACACCTCAA	2520

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GATGAATAAT AATTCACAAA ATTTCTGTGA AATCAAATCC AGTTTAAAGA GGAGCCACTT 2580

ATCAAAGAGA TTTTAACAGT AGTAAGAAGG CAAAGAATAA ACATTTGATA TTCAGCAACT 2640

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(2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 199 amino acids
 (B) TYPE: Amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
 1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
 20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
 35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
 50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
 145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
 165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
 180 185 190

Arg Leu Thr Asp Val Thr Leu
 195

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(A) LENGTH: 17 base pairs

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

17

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(A) LENGTH: 17 base pairs

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

17

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